

Sequence alignment of PKA isoforms across the kinase domain (positions 610-790). The alignment shows conservation patterns across different species and models. A color scale indicates conservation levels: black (highly conserved), red (conservative substitutions), blue (semi-conservative substitutions), green (non-conservative substitutions), and yellow (deletions).

Sequence alignment showing conservation of amino acids across various proteins (34853530.m, 38075057.m, MAST4.h, 34870261.m, 6678958.m, MAST2.h, 30842796.m, 9910296.m, MAST1.h, MAST3.h, 34877594.m, 31201487.i, 24664679.f, 17541448.w, 113r_PKA Ca, 1jlu_AMPK, 1mu_c_AUR1, 17567363.w, 1omw_GPRK2) from position 810 to 990. The alignment uses a color scale where black represents hydrophobicity and white represents hydrophilicity.

	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190
1200
34853530.m	NQIQQAFVERDILTFNAEN	PFVVCMYCSFETRRHLCMVMYEYVEGDCATLKMNCGLPVDMDARMYFAETVIALEYLHN	CIVHRDLKPDNLNTSMGHIKLTDGFLSKVGLMSMTNLYECH	IIEKDREPLDKVQCVTPYEIAPEVILR-QGYGPVDFWAMCILLYEFLVGCVPFFGDTPEELFCQVIS															
38075057.m	NQIQQAFVERDILTFNAEN	PFVVCMYCSFETRRHLCMVMYEYVEGDCATLKMNCGLPVDMDARMYFAETVIALEYLHN	CIVHRDLKPDNLNTSMGHIKLTDGFLSKVGLMSMTNLYECH	IIEKDREPLDKVQCVTPYEIAPEVILR-QGYGPVDFWAMCILLYEFLVGCVPFFGDTPEELFCQVIS															
MAST4.h	NQIQQAFVERDILTFNAEN	PFVVCMYCSFETRRHLCMVMYEYVEGDCATLKMNCGLPVDMDARMYFAETVIALEYLHN	CIVHRDLKPDNLNTSMGHIKLTDGFLSKVGLMSMTNLYECH	IIEKDREPLDKVQCVTPYEIAPEVILR-QGYGPVDFWAMCILLYEFLVGCVPFFGDTPEELFCQVIS															
34870261.m	NQIQQAFVERDILTFNAEN	PFVVCMFCSFETKRHLCMVMYEYVEGDCATLLKNICGLPVDMLRYFAETVIALEYLHN	CIVHRDLKPDNLNTSMGHIKLTDGFLSKIQGLMSLTNLYECH	IIEKDREPLDKVQCVTPYEIAPEVILR-QGYGPVDFWAMCILLYEFLVGCVPFFGDTPEELFCQVISGSFFLT															
6678958.m	NQIQQAFVERDILTFNAEN	PFVVCMFCSFETKRHLCMVMYEYVEGDCATLLKNICGLPVDMLRYFAETVIALEYLHN	CIVHRDLKPDNLNTSMGHIKLTDGFLSKIQGLMSLTNLYECH	IIEKDREPLDKVQCVTPYEIAPEVILR-QGYGPVDFWAMCILLYEFLVGCVPFFGDTPEELFCQVIS															
MAST2.h	NQIQQAFVERDILTFNAEN	PFVVCMFCSFETRRHLCMVMYEYVEGDCATLLKNICGLPVDMLRYFAETVIALEYLHN	CIVHRDLKPDNLNTSMGHIKLTDGFLSKIQGLMSLTNLYECH	IIEKDREPLDKVQCVTPYEIAPEVILR-QGYGPVDFWAMCILLYEFLVGCVPFFGDTPEELFCQVIS															
30842796.m	NQIQQAFVERDILTFNAEN	PFVVCMFCSFETRRHLCMVMYEYVEGDCATLLKNICGLPVEAMARMYFAETVIALEYLHN	CIVHRDLKPDNLNTSMGHIKLTDGFLSKIQGLMSLTNLYECH	IIEKDREPLDKVQCVTPYEIAPEVILR-QGYGPVDFWAMCILLYEFLVGCVPFFGDTPEELFCQVIS															
9910296.m	NQIQQAFVERDILTFNAEN	PFVVCMFCSFETRRHLCMVMYEYVEGDCATLLKNICGLPVEAMARMYFAETVIALEYLHN	CIVHRDLKPDNLNTSMGHIKLTDGFLSKIQGLMSLTNLYECH	IIEKDREPLDKVQCVTPYEIAPEVILR-QGYGPVDFWAMCILLYEFLVGCVPFFGDTPEELFCQVIS															
MAST1.h	NQIQQAFVERDILTFNAEN	PFVVCMFCSFETRRHLCMVMYEYVEGDCATLLKNICGLPVEAMARMYFAETVIALEYLHN	CIVHRDLKPDNLNTSMGHIKLTDGFLSKIQGLMSLTNLYECH	IIEKDREPLDKVQCVTPYEIAPEVILR-QGYGPVDFWAMCILLYEFLVGCVPFFGDTPEELFCQVIS															
MAST3.h	NQIQQAFVERDILTFNAEN	PFVVCMFCSFETRRHLCMVMYEYVEGDCATLLKNICGLPVDMDARLYFAETVIALEYLHN	CIVHRDLKPDNLNTSMGHIKLTDGFLSKIQGLMSLTNLYECH	IIEKDREPLDKVQCVTPYEIAPEVILR-QGYGPVDFWAMCILLYEFLVGCVPFFGDTPEELFCQVVS															
34877594.m	NQIQQAFVERDILTFNAEN	PFVVCMFCSFETRRHLCMVMYEYVEGDCATLLKNICGLPVDMDARLYFAETVIALEYLHN	CIVHRDLKPDNLNTSMGHIKLTDGFLSKIQGLMSLTNLYECH	IIEKDREPLDKVQCVTPYEIAPEVILR-QGYGPVDFWAMCILLYEFLVGCVPFFGDTPEELFCQVVS															
31201487.i	NOVEQFVERDILSFAIDN	PFVVCMYCSFTKKHLCLVMYEYVEGDCATLLKNICGLPDMARFYFAETVIALEYLHN	CIVHRDLKPDNLNTSMGHIKLTDGFLSKIQGLMSLTNLYECH	IIEKDREPLDKVQCVTPYEIAPEVILR-QGYGPVDFWAMCILLYEFLVGCVPFFGDTPEELFAHTVN															
24664679.f	NOVEQFVERDILSFAIDN	PFVVCMYCSFTKKHLCLVMYEYVEGDCATLLKNICGLPDMARFYFAETVIALEYLHN	CIVHRDLKPDNLNTSMGHIKLTDGFLSKIQGLMSLTNLYECH	IIEKDREPLDKVQCVTPYEIAPEVILR-QGYGPVDFWAMCILLYEFLVGCVPFFGDTPEELFAHTVN															
17541448.w	NOVEQFVERDILTMADN	PFVVCMYCSFTQYQLCMLMEYVEGDCATLLKNICGLPDMARFYFAETVIALEYLHN	CIVHRDLKPDNLNTSMGHIKLTDGFLSKIQGLMSLTNLYECH	IIEKDREPLDKVQCVTPYEIAPEVILR-QGYGPVDFWAMCILLYEFLVGCVPFFGDTPEELFAHTVN															
113_r_PKA_C	KOIEHTTNEKRLGDAVNF	PLFLKLETSFKDNSLNLYMVMEYVCGEMESLRRIEPRSEPHARFVAAICIVLDEPEYLHSDLIYRDLKPEENLIDDOQGYIQVTDGFBKAR	VKGRTIX-LCCTPEYLAPELILS-KAYNKAVDITWLGVLIYMAAGYPPFFADPIDIYFKEIVS																
1jlu_AMPK	KOIEHTTNEKRLGDAVNF	PLFLKLETSFKDNSLNLYMVMEYVCGEMESLRRIEPRSEPHARFVAAICIVLDEPEYLHSDLIYRDLKPEENLIDDOQGYIQVTDGFBKAR	VKGRTIX-LCCTPEYLAPELILS-KAYNKAVDITWLGVLIYMAAGYPPFFADPIDIYFKEIVS																
1muo_AUR1	GVEQLRERBEIISLHRH	PFEMKMSYSFTOKRHLVFMAGFCQGDMLTMIMENCEIIEERSAHFLCIVLVEGCIKTCIVHDLVLELNLNGHMIDTYLISLA	CDAEDAIQGVICRTPEYLAPELILS-KAYKGTSCTWAVGTCYCMRSDDKAVADEWSKPSYSDSTAK																
17567363.w	KHKDMEHEKILITIEN	PFEMKMSYSFTOKRHLVFMAGFCQGDMLTMIMENCEIIEERSAHFLCIVLVEGCIKTCIVHDLVLELNLNGHMIDTYLISLA	CDAEDAIQGVICRTPEYLAPELILS-KAYKGTSCTWAVGTCYCMRSDDKAVADEWSKPSYSDSTAK																
1omw_GPRK2	QGETLAINERHMLSLVSTGDCPFIIVOMSYAFTIDPKLNSFILELMNGGLDHYHLSQHFTSEADNRFPYAPCHLNLDECHVRIISDIFLACDFD-	KKKPHASVGTHYMAPEVLKGVAYDSADPFSLLCQHLPKLGCHSPFRQHKTQKHEIDRMT																	



